75703

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From: Gibbs, Terra
Sent: Friday, September 13, 2002 1:41 PM
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Subject: Sequence Search

Could you please search SEQ ID NO: 3 of serial number 10/003354

Please do a length limited search of 50 nucleotides or less. Also no EST's.

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

THANK YOU!

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/14/02
Date Completed: 9/18/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 101
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 22:59:43 ; Search time 4476.82 Seconds
(without alignments)
17356.121 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacaggccgtggttagg.....aaactttaatgagttattta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28.8	0.8	49	6	A59476	A59476 Sequence 26
2	28.8	0.8	49	6	A59509	A59509 Sequence 59
3	22.6	0.6	50	6	AX156774	AX156774 Sequence
4	22.2	0.6	50	23	E09698	E09698 Rigand whic
c 5	21.4	0.6	35	6	A84538	A84538 Sequence 10
6	21.4	0.6	38	6	AX352053	AX352053 Sequence
7	21.2	0.6	50	6	AX159492	AX159492 Sequence
8	21.2	0.6	50	6	AX159494	AX159494 Sequence
9	21.2	0.6	50	6	AX159496	AX159496 Sequence
c 10	21	0.6	43	6	AR069130	AR069130 Sequence
11	21	0.6	45	6	AX172348	AX172348 Sequence
12	20.8	0.6	32	6	I32124	I32124 Sequence 14
c 13	20.8	0.6	50	6	AX161426	AX161426 Sequence
c 14	20.8	0.6	50	6	AX199596	AX199596 Sequence
c 15	20.6	0.6	41	6	AX040470	AX040470 Sequence
c 16	20.6	0.6	45	6	AR139083	AR139083 Sequence
c 17	20.6	0.6	48	6	AX229236	AX229236 Sequence
c 18	20.6	0.6	50	6	AX164855	AX164855 Sequence
c 19	20.4	0.5	44	11	HUMUT6082A	L30452 Human STS U
20	20.4	0.5	46	6	AX287580	AX287580 Sequence
21	20.4	0.5	47	6	AX114371	AX114371 Sequence
22	20.4	0.5	50	6	AR059785	AR059785 Sequence
c 23	20.4	0.5	50	6	AX160060	AX160060 Sequence
c 24	20.4	0.5	50	6	AX160062	AX160062 Sequence
25	20.2	0.5	40	6	AX299737	AX299737 Sequence
c 26	20.2	0.5	40	6	E04963	E04963 DNA sequenc
27	20.2	0.5	40	9	S80703	S80703 gamma delta
28	20.2	0.5	46	6	I42426	I42426 Sequence 17
c 29	20.2	0.5	47	6	BD004193	BD004193 RNP deriv
30	20.2	0.5	47	6	BD004194	BD004194 RNP deriv
c 31	20.2	0.5	48	6	AX221459	AX221459 Sequence
c 32	20.2	0.5	48	6	AX221866	AX221866 Sequence
c 33	20.2	0.5	48	6	AX229252	AX229252 Sequence
c 34	20.2	0.5	50	6	AR032844	AR032844 Sequence
35	20.2	0.5	50	6	AR032964	AR032964 Sequence
36	20.2	0.5	50	6	AR032965	AR032965 Sequence
37	20.2	0.5	50	6	AX158192	AX158192 Sequence
38	20.2	0.5	50	6	AX261361	AX261361 Sequence
c 39	20.2	0.5	50	6	I29584	I29584 Sequence 45
40	20.2	0.5	50	6	I29704	I29704 Sequence 57
41	20.2	0.5	50	6	I29705	I29705 Sequence 57
c 42	20.2	0.5	50	6	I36502	I36502 Sequence 1
c 43	20.2	0.5	50	6	I91258	I91258 Sequence 45
44	20.2	0.5	50	6	I91378	I91378 Sequence 57
45	20.2	0.5	50	6	I91379	I91379 Sequence 57

ALIGNMENTS

RESULT 1
A59476
LOCUS A59476 49 bp DNA linear PAT 06-MAR-1998
DEFINITION Sequence 26 from Patent WO9705234.
ACCESSION A59476
VERSION A59476.1 GI:3714788
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS Chamberlain,S., Pook,M.A., Doudney,C., William,E., Hillermann,R., Garcia-Valdecasas,J.J. and C.
TITLE GENE FOR FRIEDREICH'S ATAXIA
JOURNAL Patent: WO 9705234-A 26 13-FEB-1997;
IMPERIAL COLLEGE (GB)
FEATURES Location/Qualifiers
source 1. .49
/organism="unidentified"
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BASE COUNT 15 a 5 c 13 g 16 t
ORIGIN

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  Best Local Similarity   75.0%;  Pred. No. 1.4e+04;
  Matches   36;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   1591 gtttgttaagaagttggagcactcttggaaagccctggtacatgacgg 1638
          |||  | |||||||| || || || |||||||| || ||  |||| ||
Db      1 GTTAATGAAGAAGTTAGAACATTCCTGGAAAGCTCTTGTTTATGATGG 48


RESULT   2
A59509
LOCUS       A59509                   49 bp    DNA     linear   PAT 06-MAR-1998
DEFINITION  Sequence 59 from Patent WO9705234.
ACCESSION   A59509
VERSION     A59509.1  GI:3714821
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Chamberlain,S., Pook,M.A., Doudney,C., William,E., Hillermann,R.,
            Garcia-Valdecasas,J.J. and C.
  TITLE     GENE FOR FRIEDREICH'S ATAXIA
  JOURNAL   Patent: WO 9705234-A 59 13-FEB-1997;
            IMPERIAL COLLEGE (GB)
FEATURES             Location/Qualifiers
     source          1. .49
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                     /db_xref="taxon:32644"
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  Query Match             0.8%;  Score 28.8;  DB 6;  Length 49;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+04;
  Matches   36;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   1591 gtttgttaagaagttggagcactcttggaaagccctggtacatgacgg 1638
          |||  | |||||||| || || || |||||||| || ||  |||| ||
Db      1 GTTAATGAAGAAGTTAGAACATTCCTGGAAAGCTCTTGTTTATGATGG 48


RESULT   3
AX156774
LOCUS       AX156774                 50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 102 from Patent WO0140521.
ACCESSION   AX156774
VERSION     AX156774.1  GI:14538105
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 102 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43294390"
     misc_feature    26
                     /note="2 of 2 allelic variants (101 is other entry)"
BASE COUNT        8 a     10 c      3 g     29 t
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  Best Local Similarity   75.7%;  Pred. No. 7.4e+05;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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          | |  |||||||| ||||||||||   | || ||||
Db      1 TTCTTGCTTTCTTTTTCTTTTTTTTCAATAAACAAAG 37


RESULT   4
E09698
ID   E09698     standard; DNA; UNC; 50 BP.
XX
AC   E09698;
XX
SV   E09698.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   Rigand which is part of IgE receptor beta chain gene.
XX
KW   JP 1995194400-A/11.
XX
OS   unidentified
OC   unclassified.
XX
RN   [1]
RP   1-50
RA   Ozoegawa M., Miyabe Y., Nakada M., Ra T., Suzuki K.;
RT   "DNA PROBE FOR DETECTING ALLERGIC DISEASE AND METHOD FOR DETECTING ALLERGIC
RT   DISEASE GENE USING THE SAME";
RL   Patent number JP1995194400-A/11, 01-AUG-1995.
RL   SUMITOMO ELECTRIC IND LTD.
XX
CC   OS   None
CC   OC   Artificial sequences.
CC   PN   JP 1995194400-A/11
CC   PD   01-AUG-1995
CC   PF   21-OCT-1994 JP 1994282915
CC   PR   22-OCT-1993 JP 93P   265144
CC   PI   OZOEGAWA MISAKO, MIYABE YUKI, NAKADA MOTOMI, RA TOMOYASU,
CC   PI   SUZUKI KATSUHIRO
CC   PC   C12Q1/68,G01N33/50//C12N15/09;
CC   CC   strandedness: Single;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .50
CC   FT                   /organism="Artificial sequences"
CC   FT   misc_feature    1. .50
CC   FT                   /note="Rigand which is part of IgE receptor
CC   FT                   beta chain
CC   FT                   gene"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .50
FT                   /db_xref="taxon:32644"
FT                   /organism="unidentified"
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SQ   Sequence 50 BP; 12 A; 17 C; 10 G; 11 T; 0 other;


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  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   2256 cagagagttgaggaccgcagcatccccctccactccagagttgg 2298
          ||||  |||| | | ||  ||||||| ||||| || |  |||
Db      8 CAGACTATTGAAGTCGGCCTCATCCCCACCACTGCATACATGG 50
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RESULT   5
A84538/c
LOCUS       A84538                    35 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 10 from Patent WO9845476.
ACCESSION   A84538
VERSION     A84538.1  GI:6733457
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Schweizer,M.
  TITLE     BIOLOGICAL ASSAY FOR TESTING THE CARCINOGENIC PROPERTIES OF A
            SUBSTANCE
  JOURNAL   Patent: WO 9845476-A 10 15-OCT-1998;
            INST OF FOOD RESEARCH (GB); SCHWEIZER MICHAEL (GB)
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unidentified"
                     /db_xref="taxon:32644"
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ORIGIN

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  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2561 cccagctttcttcttcttttttttttctgaa 2591
          ||  ||||| || || ||||||||||| |||
Db     33 CCGGGCTTTTTTTTTTTTTTTTTTTCCGAA 3


RESULT   6
AX352053
LOCUS       AX352053                  38 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 349 from Patent WO0193902.
ACCESSION   AX352053
VERSION     AX352053.1  GI:18617336
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 349 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
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ORIGIN


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  Best Local Similarity   80.6%;  Pred. No. 1.5e+06;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1221 tacaagacatccctgatggtctttttttgga 1251
          | || ||| | ||||||| | ||||||||||
Db      1 TCCATGACGTTCCTGATGCTTTTTTTTTGGA 31


RESULT   7
AX159492
LOCUS       AX159492                  50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2820 from Patent WO0140521.
ACCESSION   AX159492
VERSION     AX159492.1  GI:14540823
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 2820 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg42513366"
     misc_feature    26
                     /note="2 of 2 allelic variants (2819 is other entry)"
BASE COUNT       10 a      7 c      7 g     26 t
ORIGIN


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  Matches   26;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2564 agctttcttcttcttttttttttctgaaaaaagg 2597
          || || ||| || |||||||||| | | | ||||
Db      3 AGTTTGCTTTTTGTTTTTTTTTTTTAAGACAAGG 36


RESULT   8
AX159494
LOCUS       AX159494                  50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2822 from Patent WO0140521.
ACCESSION   AX159494
VERSION     AX159494.1  GI:14540825
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 2822 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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                     /note="2 of 2 allelic variants (2821 is other entry)"
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ORIGIN


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  Matches   26;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2564 agctttcttcttcttttttttttctgaaaaaagg 2597
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Db      2 AGTTTGCTTTTTGTTTTTTTTTTTTAAGACAAGG 35
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RESULT  9
AX159496
LOCUS       AX159496                 50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2824 from Patent WO0140521.
ACCESSION   AX159496
VERSION     AX159496.1  GI:14540827
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 2824 07-JUN-2001;
            Curagen Corporation (US)
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                     Accession number cg42513366"
     misc_feature    26
                     /note="2 of 2 allelic variants (2823 is other entry)"
BASE COUNT        8 a      9 c      7 g     26 t
ORIGIN


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  Matches   26;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2564 agctttcttctttttttttttctgaaaaaagg 2597
           || || ||| || |||||||||| | | | ||||
Db      1 AGTTTGCTTTTTGTTTTTTTTTTTTAAGACAAGG 34


RESULT  10
AR069130/c
LOCUS       AR069130                 43 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 14 from patent US 5891439.
ACCESSION   AR069130
VERSION     AR069130.1  GI:7220018
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Vaidya,T., Bakhiet,A., Olsson,T., Kristensson,K. and Donelson,J.E.
  TITLE     Lymphocyte stimulating factor
  JOURNAL   Patent: US 5891439-A 14 06-APR-1999;
FEATURES             Location/Qualifiers
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BASE COUNT       24 a      7 c      1 g     11 t
ORIGIN


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           ||| || || |||||||||  |||||  |  | ||||
Db     42 TTTTTTTTTTTTTTTTTTTAGTGAAATGACAATAAAG 6


RESULT  11
AX172348
LOCUS       AX172348                 45 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0144811.
ACCESSION   AX172348
VERSION     AX172348.1  GI:14597500
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Singh,S., Pease,J.S., Sadakian,J., Wagner,D.B. and Ullman,E.F.
  TITLE     Light-emitting particles for diagnostic and therapeutic use
  JOURNAL   Patent: WO 0144811-A 1 21-JUN-2001;
            DADE BEHRING INC. (US)
FEATURES             Location/Qualifiers
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Qy   2568 ttcttcttctttttttttttctgaaaaaaggaaaaagcacacagca 2612
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Db      1 TTTTTTTTTTTTTTTTTTTTGTTAAAAGAGACCATCAATGAGGA 45


RESULT  12
I32124
LOCUS       I32124                   32 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5585242.
ACCESSION   I32124
VERSION     I32124.1  GI:1822915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Bouma,S.R., Khalil,O.S. and Pabich,E.K.
  TITLE     Method for detection of nucleic acid using total internal
            reflectance
  JOURNAL   Patent: US 5585242-A 14 17-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT        0 a      7 c      3 g     22 t
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Qy   2555 ccacctcccagctttcttcttctttttttttt 2586
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Db      1 CCGCCTGTCCGCTTTTTTTTTTTTTTTTTT 32


RESULT  13
AX161426/c
LOCUS       AX161426                 50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4754 from Patent WO0140521.
ACCESSION   AX161426
VERSION     AX161426.1  GI:14542757
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
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  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 4754 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43969665"
     misc_feature    26
                     /note="2 of 2 allelic variants (4753 is other entry)"
BASE COUNT       20 a      6 c     12 g     12 t
ORIGIN


  Query Match             0.6%;  Score 20.8;  DB 6;  Length 50;
  Best Local Similarity   78.1%;  Pred. No. 2.3e+06;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   3682 ttttaatgtaataaactttaatgagttattta 3713
          ||||  || ||  ||||||||||| || ||||
Db     50 TTTTTCTGCAAGCAACTTTAATGACTTTTTTA 19

RESULT  14
AX199596/c
LOCUS       AX199596                 50 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 526 from Patent WO0151670.
ACCESSION   AX199596
VERSION     AX199596.1  GI:15390030
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.D.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0151670-A 526 19-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg42855114"
     misc_feature    26
                     /note="2 of 2 allelic variants (525 is other entry)"
BASE COUNT       20 a      8 c     10 g     12 t
ORIGIN


  Query Match             0.6%;  Score 20.8;  DB 6;  Length 50;
  Best Local Similarity   64.6%;  Pred. No. 2.3e+06;
  Matches   31;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy   2307 gattttcaactggccaacccttgcctccactattgaatttttttcag 2354
          || ||||| ||    | |    || | ||| | ||| |||||||| |
Db     48 GAGTTTCATCTTCTGACCAGGATGACACCAATTTTGCATTTTTTTCTG 1


RESULT  15
AX040470/c
LOCUS       AX040470                 41 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 10 from Patent WO0063365.
ACCESSION   AX040470
VERSION     AX040470.1  GI:11230262
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Belotserkovskii,B., Reddy,G. and Zarling,D.
  TITLE     Locked nucleic acid hybrids and methods of use
  JOURNAL   Patent: WO 0063365-A 10 26-OCT-2000;
            Pangene Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Triplex forming DNA"
BASE COUNT       7 a     25 c      2 g      7 t
ORIGIN


  Query Match             0.6%;  Score 20.6;  DB 6;  Length 41;
  Best Local Similarity   74.3%;  Pred. No. 2.6e+06;
  Matches   26;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   3566 ggagggctgggtcttagggaaaggaatggggaagc 3600
          || |||  |||| |||||| | |||   |||||||
Db     36 GGTGGGTGGGGTATTAGGGGAGGGAGGAGGGAAGC 2


Search completed: September 18, 2002, 01:15:45
Job time: 8162 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 23:03:38 ; Search time 382.89 Seconds
(without alignments)
16649.438 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacaggccgtggttagg.....aaactttaatgagttattta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	28.8	0.8	49	18	AAT84374	Friedreich's ataxi
c	2	24.8	0.7	50	22	AAL30887	Human SNP oligonuc
	3	24.6	0.7	50	22	AAL31735	Human SNP oligonuc
	4	22.6	0.6	45	16	AAQ99068	(Ser4Gly)2 linker
	5	22.6	0.6	45	21	AAA12866	DNA encoding (Ser4
	6	22.6	0.6	50	22	AAI73161	Human silent SNP c
	7	22.2	0.6	40	22	AAH20340	HHV6 virus p41 gen
	8	22.2	0.6	48	22	AAL30218	Human SNP oligonuc
	9	22.2	0.6	50	16	AAQ87804	IgE receptor beta
	10	22	0.6	48	16	AAT04081	Trypsin inhibitory
	11	22	0.6	50	22	AAL34072	Human SNP oligonuc
	12	21.8	0.6	50	22	AAL28913	Human SNP oligonuc
	13	21.6	0.6	40	22	AAH20339	HHV6 virus p41 gen
c	14	21.6	0.6	50	22	AAL31293	Human SNP oligonuc
c	15	21.4	0.6	35	20	AAV83644	Oligonucleotide us
	16	21.2	0.6	47	22	AAL30217	Human SNP oligonuc
c	17	21.2	0.6	50	22	AAL27921	Human SNP oligonuc
c	18	21.2	0.6	50	22	AAL28580	Human SNP oligonuc
	19	21.2	0.6	50	22	AAI75879	Human silent SNP c
	20	21.2	0.6	50	22	AAI75881	Human silent SNP c
	21	21.2	0.6	50	22	AAI75883	Human silent SNP c
	22	21	0.6	44	22	AAL28737	Human SNP oligonuc
	23	21	0.6	45	20	AAZ31524	Probe for HIV RNA
	24	21	0.6	45	20	AAZ11012	Probe #1 for HIV t
	25	21	0.6	45	22	AAD18751	Probe #1 used for
c	26	21	0.6	46	20	AAX77169	Chimeric packaging
c	27	20.8	0.6	47	21	AAZ67568	Human map-related
c	28	20.8	0.6	50	22	AAL28914	Human SNP oligonuc
c	29	20.8	0.6	50	22	AAI77813	Human silent SNP c
c	30	20.8	0.6	50	22	AAH89745	Human coding sequ
	31	20.6	0.6	27	20	AAX23570	Deletion sequence
c	32	20.6	0.6	41	21	AAC66740	Probe pTL. Uniden
	33	20.6	0.6	45	16	AAQ80709	Drosophila hsp70 g
c	34	20.6	0.6	45	22	AAC89633	S. cerevisiae YKR0
c	35	20.6	0.6	47	21	AAZ67659	Human map-related
c	36	20.6	0.6	48	22	AAH97394	Human Chk1 ribozym
c	37	20.6	0.6	50	22	AAL29036	Human SNP oligonuc
	38	20.6	0.6	50	22	AAL30220	Human SNP oligonuc
c	39	20.6	0.6	50	23	ABL00059	Human silent nonco
	40	20.4	0.5	40	15	AAQ55168	Sequence of primer
	41	20.4	0.5	41	20	AAX34851	Primer for adapter
	42	20.4	0.5	41	20	AAX23455	Human neutrophil c
	43	20.4	0.5	46	24	AAS95733	Allele discriminat
c	44	20.4	0.5	47	21	AAZ67078	Human map-related
c	45	20.4	0.5	47	21	AAZ67213	Human map-related

ALIGNMENTS

RESULT 1
AAT84374
ID AAT84374 standard; DNA; 49 BP.
XX
AC AAT84374;
XX
DT 12-NOV-1997 (first entry)
XX
DE Friedreich's ataxia STM7 gene exon 11.
XX
KW STM7.I gene; Friedreich's ataxia; FRDA; neurodegeneration;
KW phosphatidylinositol-4-phosphate 5-kinase; PtdInsP5K;
KW transgenic animal; animal model; diagnosis; therapy;
KW STM7.IIIa; STM7.IIIb; STM7.IIIc; ss.
XX
OS Homo sapiens.
XX
PN WO9705234-A2.
XX
PD 13-FEB-1997.
XX
PF 24-JUL-1996; 96WO-GB01786.
XX
PR 28-JUL-1995; 95GB-0015508.
PR 26-JUL-1995; 95GB-0015309.
XX
PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI Chamberlain S, Doudney CWE, Garcia-Valdecasas JJC;
PI Hillermann R, Pook MA;
XX
DR WPI; 1997-145674/13.

XX
PT New gene, STM7, and new protein causing Friedreich's Ataxia -
PT encodes phosphatidylinositol phosphate kinase isoform; also splice
PT variants and transgenic animals, for diagnosing pre-disposition to
PT Friedreich's ataxia
XX
PS Claim 1; Fig 16; 82pp; English.
XX
CC DNA sequences (AAT84364-86) are provided for exons 1-23,
CC respectively, of the human STM7 gene associated with Friedreich's
CC ataxia (FRDA). The STM7.I gene (see AAT84358) comprises exons
CC 1-16 of the gene, while splice variant STM7.IIIa includes exons
CC 1-13, 17 and 19-22, splice variant STM7.IIIb includes exons
CC 1-15, 17, 19, 21-22 and splice variant STM7.IIIc includes exons
CC 1-15 and 19-22. STM7 nucleic acids can be used to produce STM7
CC polypeptides (see AAW00978) in transfected host cells, to design
CC probes (esp. oligonucleotides from exons 1-16, partic. 7-11) used
CC in a claimed method for determining an inherited predisposition to
CC FRDA, to generate transgenic animal models of FRDA and in somatic
CC cell therapy.
XX
SQ Sequence 49 BP; 15 A; 5 C; 13 G; 16 T; 0 other;

Query Match 0.8%; Score 28.8; DB 18; Length 49;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1591 gtttgttaagaagttggagcactcttggaaagccctggtacatgacgg 1638
||| | |||||||| || || || |||||||| || || |||| ||
Db 1 gttaatgaagaagttagaacattcctggaaagctcttgtttatgatgg 48

RESULT 2
AAL30887/c
ID AAL30887 standard; DNA; 50 BP.
XX
AC AAL30887;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4095.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2562; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 16 A; 3 C; 6 G; 25 T; 0 other;

Query Match 0.7%; Score 24.8; DB 22; Length 50;
Best Local Similarity 72.7%; Pred. No. 5.5e+03;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2577 ttttttttttctgaaaaaaggaaaaagcacacagcacacaattt 2620
| |||||||| ||||||| ||||| ||| | ||||| ||
Db 44 TCTTTTTTTTAAAAAAAAAGCAAAAAAGACATACAACACATATT 1

RESULT 3
AAL31735
ID AAL31735 standard; DNA; 50 BP.
XX
AC AAL31735;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4943.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2809; 4143pp; English.
XX

```
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 50 BP; 11 A; 8 C; 4 G; 27 T; 0 other;


  Query Match             0.7%;  Score 24.6;  DB 22;  Length 50;
  Best Local Similarity   87.1%;  Pred. No. 6.3e+03;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    2566 ctttcttcttcttttttttttctgaaaaaag 2596
           |||| || || |||||||||| |||||||||
Db       3 ctttattattatttttttttttgaaaaaag 33


RESULT   4
AAQ99068
ID   AAQ99068 standard; cDNA; 45 BP.
XX
AC   AAQ99068;
XX
DT   13-MAY-1996  (first entry)
XX
DE   (Ser4Gly)2 linker used in FGF/saporin fusion protein, FPFS11.
XX
KW   Conjugate; fibroblast growth factor; FGF; cytotoxin; saporin; eye;
KW   cell proliferation; regulation; pterygia; corneal clouding; cancer;
KW   psoriasis; rheumatoid arthritis; ss.
XX
OS   Synthetic.
XX
PN   WO9524928-A2.
XX
PD   21-SEP-1995.
XX
PF   15-MAR-1995;   95WO-US03448.
XX
PR   15-MAR-1994;   94US-0213447.
PR   15-MAR-1994;   94US-0213446.
XX
PA   (PRIZ-) PRIZM PHARM INC.
XX
PI   Baird JA,  Houston LL,  Nova MP,  Sosnowski BA;
XX
DR   WPI; 1995-336820/43.
XX
PT   New conjugates of growth factor receptor ligand and targetted agent
PT   - partic. DNA or cytotoxin, used to control cell proliferation in
PT   the eye, e.g. to prevent growth of pterygii and corneal clouding
XX
PS   Claim 5; Page 110; 204pp; English.
XX
CC   AAQ99068 is a (Ser4Gly)2 substrate linker which is used in a fibroblast
CC   growth factor (FGF)/saporin fusion protein (FP) to increase FP
CC   flexibility. DNA sequences encoding FGF/saporin fusion proteins are
CC   useful for targetting saporin to a cell carrying the FGF receptor.
CC   Sequences used to link together FGFs and other sequences which may
CC   be beneficially targetted to a cell (targetted agents, TA) may be
CC   linked by a sequence which can increase serum stability or
CC   intracellular availability of the TA. The conjugates of the invention
CC   are used to inhibit  cell proliferation in cells carrying the
CC   particular growth factor receptor; also when TA is DNA it can be used
CC   to deliver this to cells (for gene therapy). A specific application
CC   is to prevent excessive proliferation of epithelial cells,
CC   fibroblasts and keratinocytes in the anterior eye after surgery,
CC   partic. to prevent recurrence of pterygii after surgical removal,
CC   closure of trabeculectomy after glaucoma surgery and corneal clouding
CC   after excimer laser treatment. Other conditions which may be treated
CC   include tumours, restenosis, psoriasis, Dupuytren's contracture,
CC   diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.
XX
SQ   Sequence 45 BP; 2 A; 16 C; 17 G; 10 T; 0 other;


  Query Match             0.6%;  Score 22.6;  DB 16;  Length 45;
  Best Local Similarity   75.7%;  Pred. No. 2.2e+04;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    401 atggcgtcggcctcctccgggccgtcgtcttcggtcg 437
          ||||| ||| | || || ||  ||||||| |||| ||
Db      3 atggcctcgtcgtcgtcgggctcgtcgtcgtcgggcg 39


RESULT   5
AAA12866
ID   AAA12866 standard; DNA; 45 BP.
XX
AC   AAA12866;
XX
DT   18-JUL-2000  (first entry)
XX
DE   DNA encoding (Ser4-Gly)2 flexible linker peptide, SEQ ID NO:50.
XX
KW   Targetted gene delivery; fibroblast growth factor receptor;
KW   FGFR-binding protein; nucleic acid binding protein;
KW   receptor-internalised ligand; cytotoxin; saporin; gene therapy;
KW   cytocide; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW   rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;
KW   eczema; nuclear translocation signal; NTS;
KW   cytoplasmic translocation signal; endosome-disruptive peptide; ss.
XX
OS   Synthetic.
XX
PN   US6037329-A.
XX
PD   14-MAR-2000.
XX
PF   24-SEP-1996;   96US-0718904.
XX
PR   15-MAR-1994;   94US-0213446.
PR   15-MAR-1994;   94US-0213447.
PR   29-AUG-1994;   94US-0297961.
PR   13-SEP-1994;   94US-0305771.
PR   16-MAY-1995;   95US-0441979.
XX
PA   (SELE-) SELECTIVE GENETICS INC.
XX
PI   Chandler LA,  Sosnowski BA,  Baird JA;
XX
DR   WPI; 2000-292008/25.
XX
PT   Gene delivery system, useful for treating or preventing cancer and
PT   rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT   nucleic acid binding domain and nucleic acid  -
XX
PS   Claim 21; Column 33; 131pp; English.
XX
CC   The invention relates to a novel gene delivery composition for the
CC   targetted delivery of cytotoxins or prodrug-converting enzymes to
CC   proliferating cells. The gene delivery composition comprises a protein
CC   that binds the fibroblast growth factor receptor (FGFR) which is fused
CC   or chemically conjugated to a nucleic acid binding domain. The nucleic
```

CC acid binding domain is complexed with a suitable expression construct
CC encoding a cytotoxin such as saporin. One or more linkers may join the
CC FGFR-binding protein to the nucleic acid binding protein. These are
CC selected to increase the specificity, toxicity, solubility, serum
CC stability or intracellular availability, and may serve to promote
CC condensation of nucleic acids for delivery to a cell. The fusion protein
CC binds to FGFR and is internalised by cells that carry this receptor. The
CC gene delivery composition is used for the therapeutic alteration of the
CC function, gene expression and viability of cells. In particular, it may
CC be used for the treatment and prevention of cell proliferative
CC disorders, for example after eye surgery, melanoma and many other sorts
CC of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC diabetic retinopathy, psoriasis and eczema. The gene delivery
CC compositions of the invention have high specificity for particular cells
CC and can deliver larger amounts of DNA compared to prior art methods.
CC Sequences AAY90424- AAY90441 represent nuclear translocation signals
CC (NTSs) from a variety of proteins, and AAY90442-Y90444 represent
CC cytoplasmic translocation signals. Sequences AAY90445-Y90446 are
CC endosome-disruptive peptides. Sequences AAA12863-A12867 encode flexible
CC linker peptides, AAY90447 being a claimed linker peptide. AAA12882-A12887
CC encode linkers that are substrates for certain enzymes, AAY90451-Y90453
CC being examples of such linkers.
XX
SQ Sequence 45 BP; 2 A; 16 C; 17 G; 10 T; 0 other;

Query Match 0.6%; Score 22.6; DB 21; Length 45;
Best Local Similarity 75.7%; Pred. No. 2.2e+04;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 401 atggcgtcggcctcctccgggccgtcgtcttcggtcg 437
|||||| ||| | || || || ||||||| |||| ||
Db 3 atggcctcgtcgtcgtcgggctcgtcgtcgtcgggcg 39

RESULT 6
AAI73161
ID AAI73161 standard; DNA; 50 BP.
XX
AC AAI73161;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:102.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 85; 2653pp; English.
XX
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 50 BP; 8 A; 10 C; 3 G; 29 T; 0 other;

Query Match 0.6%; Score 22.6; DB 22; Length 50;
Best Local Similarity 75.7%; Pred. No. 2.3e+04;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2560 tcccagctttcttcttctttttttttttctgaaaaaag 2596
| | |||||||| |||||||||| | || ||||
Db 1 ttcttgctttctttttctttttttcaataaacaaag 37

RESULT 7
AAH20340
ID AAH20340 standard; DNA; 40 BP.
XX
AC AAH20340;
XX
DT 01-AUG-2001 (first entry)
XX
DE HHV6 virus p41 gene specific primer p41FH92 SEQ ID 21.
XX
KW Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS Human herpesvirus 6.
OS Synthetic.
XX
PN US6221635-B1.
XX
PD 24-APR-2001.
XX
PF 06-MAY-1999; 99US-0306290.
XX
PR 06-MAY-1999; 99US-0306290.
XX
PA (WIST-) WISTAR INST.
XX
PI Rovera G, Mukhopadhyay S;
XX
DR WPI; 2001-315577/33.
XX
PT Detecting the presence of a specific nucleic acid in a sample
PT containing DNA, useful in scanning large genomic fragments for the
PT presence of genes or gene families, comprises performing solid phase
PT amplification of DNA template -
XX
PS Example 2; Column 28; 49pp; English.
XX
CC This invention relates to a method for detecting the presence of a
CC specific nucleic acid in a sample containing DNA. The method comprises
CC performing solid phase amplification of DNA template (SPADT). 5' and 3'
CC primers are irreversible bound to a solid support, and the DNA from a
CC sample is absorbed and reversibly bound, incubated under amplification
CC reaction conditions and the presence of the specific target DNA is

```
CC   detected. The method is useful for detecting the presence of a specific
CC   nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC   cell. SPADT may be used for scanning large genomic fragments for the
CC   presence of genes or gene families; or for bacterial diagnostics by
CC   examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC   for the presence of viral nucleic acid sequences in a sample. SPADT may
CC   also be used in forensic medicine by detecting and identifying species
CC   specific sequences or for the presence of major histocompatibility
CC   complex. The present sequence represents a primer specific for the human
CC   herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC   illustrating the method of the invention.
XX
SQ   Sequence 40 BP; 9 A; 2 C; 4 G; 25 T; 0 other;


  Query Match             0.6%;  Score 22.2;  DB 22;  Length 40;
  Best Local Similarity   77.1%;  Pred. No. 2.6e+04;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2568 ttcttcttcttttttttttctgaaaaaaggaaaaa 2602
            || || || |||||||||| ||||||   | ||||
Db      1 ttttttttttttttttttttttgaaaagctggaaaa 35


RESULT   8
AAL30218
ID   AAL30218 standard; DNA; 48 BP.
XX
AC   AAL30218;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #3426.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 2369; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 48 BP; 7 A; 9 C; 1 G; 31 T; 0 other;


  Query Match             0.6%;  Score 22.2;  DB 22;  Length 48;
  Best Local Similarity   69.8%;  Pred. No. 2.9e+04;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   3473 ttgctatttttttttcataatttactatttatgatgtatttaa 3515
          ||  | |||||||||  || ||| |||  |  | | |||||||
Db      6 ttttttttttttttttttttactttcctacatcagttttatttaa 48


RESULT   9
AAQ87804
ID   AAQ87804 standard; DNA; 50 BP.
XX
AC   AAQ87804;
XX
DT   14-NOV-1995  (first entry)
XX
DE   IgE receptor beta chain ligand.
XX
KW   Probe; immunoglobulin; IgE; receptor; beta; allergic disease;
KW   detection; screening; diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "May optionally be labelled with Aminolink 2
FT                          (product of ABI company)"
XX
PN   EP649910-A.
XX
PD   26-APR-1995.
XX
PF   21-OCT-1994;   94EP-0307751.
XX
PR   22-OCT-1993;   93JP-0265144.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI   Miyabe Y,  Nakata M,  Osoegawa M,  Ra C,  Suzuki K;
XX
DR   WPI; 1995-156760/21.
XX
PT   Probes for mutation(s) in beta chain gene of a high affinity IgE
PT   receptor - for the diagnosis of allergic disease, esp. in
PT   neonate(s)
XX
PS   Claim 8; Page 8; 17pp; English.
XX
CC   DNA probes (See AAQ87799-803) having sequences identical or
CC   complementary to parts of the immunoglobulin E (IgE) receptor, are
CC   used to detect genes associated with allergic disease (diseases
CC   involving mutations in the beta chain gene).  They may be used in
CC   neonatal screening, prenatal diagnosis etc.  This sequence is an
CC   IgE ligand which is immobilised on a support and used to bind to
CC   probe/IgE receptor gene conjugates. The probe is then eluted by a
CC   gradual rise in temperature.
XX
SQ   Sequence 50 BP; 12 A; 17 C; 10 G; 11 T; 0 other;
```

```
  Query Match             0.6%;  Score 22.2;  DB 16;  Length 50;
  Best Local Similarity   69.8%;  Pred. No. 3e+04;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    2256 cagagagttgaggaccgcagcatccccctccactccagagttgg 2298
           ||||   |||| | | ||  ||||||| ||||| || |  |||
Db       8 cagactattgaagtcggcctcatccccaccactgcatacatgg 50


RESULT  10
AAT04081
ID   AAT04081 standard; DNA; 48 BP.
XX
AC   AAT04081;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Trypsin inhibitory protein cDNA antisense primer-1.
XX
KW   Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC;
KW   multiple organ failure; disseminated intravascular coagulation; ss.
XX
OS   Synthetic.
XX
PN   JP07242700-A.
XX
PD   19-SEP-1995.
XX
PF   04-MAR-1994;   94JP-0059906.
XX
PR   04-MAR-1994;   94JP-0059906.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
XX
DR   WPI; 1995-355285/46.
XX
PT   Polypeptide having trypsin inhibitory activity - for the treatment
PT   of pancreatitis, shock, multi-organ failure, etc.
XX
PS   Example 7; Page 15; 25pp; Japanese.
XX
CC   A polypeptide having trypsin inhibitory activity, mol.wt. 22-28 kD
CC   or 17-23 kD (as determined by SDS-PAGE under reducing or non-
CC   reducing conditions, respectively) and an N-terminal sequence as in
CC   AAR79913 is claimed. The polypeptide was isolated from human T98G
CC   cells and is useful for treating pancreatitis, shock, multiple
CC   organ failure and disseminated intravascular coagulation. The
CC   present sequence is that of an antisense primer used for cloning
CC   T98G cDNA coding for the full-length polypeptide.
XX
SQ   Sequence 48 BP; 2 A; 1 C; 1 G; 44 T; 0 other;


  Query Match             0.6%;  Score 22;  DB 16;  Length 48;
  Best Local Similarity   67.4%;  Pred. No. 3.3e+04;
  Matches   31;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    3467 gaattcttgctatttttttttcataatttactatttatgatgtatt 3512
           ||||||||  | |||||||||  |  |||  | ||| |  | | ||
Db       3 gaattctttttttttttttttttttttttttttttttttttttttt 48


RESULT  11
AAL34072
ID   AAL34072 standard; DNA; 50 BP.
XX
AC   AAL34072;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #7280.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 3479; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 50 BP; 17 A; 5 C; 7 G; 21 T; 0 other;


  Query Match             0.6%;  Score 22;  DB 22;  Length 50;
  Best Local Similarity   67.4%;  Pred. No. 3.4e+04;
  Matches   31;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    2564 agctttcttcttcttttttttttctgaaaaaaggaaaaagcacaca 2609
           | ||||   ||  ||||||||||| | |||  ||||  |  | | |||
Db       1 atctttaaactcatttttttttttttaaaaggaggacattgtaaaca 46


RESULT  12
AAL28913
ID   AAL28913 standard; DNA; 50 BP.
XX
AC   AAL28913;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #2121.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
```

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KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 1988; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 50 BP; 13 A; 11 C; 14 G; 12 T; 0 other;


  Query Match             0.6%;  Score 21.8;  DB 22;  Length 50;
  Best Local Similarity   78.8%;  Pred. No. 3.9e+04;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2007 ccttggaaaagcttgaagttgcagagtcagagt 2039
           ||||||||||||   |||||||  | || ||||
Db     15 ccttggaaaagccgcaagttgcttactccgagt 47


RESULT  13
AAH20339
ID   AAH20339 standard; DNA; 40 BP.
XX
AC   AAH20339;
XX
DT   01-AUG-2001  (first entry)
XX
DE   HHV6 virus p41 gene specific primer p41FH46 SEQ ID 20.
XX
KW   Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW   genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS   Human herpesvirus 6.
OS   Synthetic.
XX
PN   US6221635-B1.
XX
PD   24-APR-2001.
XX
PF   06-MAY-1999;   99US-0306290.
XX
PR   06-MAY-1999;   99US-0306290.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Rovera G,  Mukhopadhyay S;
XX
DR   WPI; 2001-315577/33.
XX
PT   Detecting the presence of a specific nucleic acid in a sample
PT   containing DNA, useful in scanning large genomic fragments for the
PT   presence of genes or gene families, comprises performing solid phase
PT   amplification of DNA template  -
XX
PS   Example 2; Column 28; 49pp; English.
XX
CC   This invention relates to a method for detecting the presence of a
CC   specific nucleic acid in a sample containing DNA. The method comprises
CC   performing solid phase amplification of DNA template (SPADT). 5' and 3'
CC   primers are irreversible bound to a solid support, and the DNA from a
CC   sample is absorbed and reversibly bound, incubated under amplification
CC   reaction conditions and the presence of the specific target DNA is
CC   detected. The method is useful for detecting the presence of a specific
CC   nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC   cell. SPADT may be used for scanning large genomic fragments for the
CC   presence of genes or gene families; or for bacterial diagnostics by
CC   examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC   for the presence of viral nucleic acid sequences in a sample. SPADT may
CC   also be used in forensic medicine by detecting and identifying species
CC   specific sequences or for the presence of major histocompatibility
CC   complex. The present sequence represents a primer specific for the human
CC   herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC   illustrating the method of the invention.
XX
SQ   Sequence 40 BP; 9 A; 3 C; 7 G; 21 T; 0 other;


  Query Match             0.6%;  Score 21.6;  DB 22;  Length 40;
  Best Local Similarity   75.0%;  Pred. No. 3.9e+04;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttctttttttttttctgaaaaaaggaaaaa 2602
           ||| || || ||||||||||| | || |  || |||
Db      1 ttttttttttttttttttttcgggaacatagagaaa 36


RESULT  14
AAL31293/c
ID   AAL31293 standard; DNA; 50 BP.
XX
AC   AAL31293;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #4501.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
```

OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2680; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 24 A; 5 C; 4 G; 17 T; 0 other;

```
  Query Match             0.6%;  Score 21.6;  DB 22;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 4.4e+04;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttctttttttttttctgaaaaaaggaaaaa 2602
          | | | |||| ||||||||| | | ||| | |||||
Db     36 TATTTACTTCCTTTTTTTTTTTAAGAAAGGAAAAAA 1
```

RESULT 15
AAV83644/c
ID AAV83644 standard; DNA; 35 BP.
XX
AC AAV83644;
XX
DT 01-MAR-1999 (first entry)
XX
DE Oligonucleotide used in the construction of assay plasmids.
XX
KW Repetitive sequence; carcinogenic; human dietary component;
KW DNA instability; cancer; diet; primer; ss.
XX
OS Synthetic.
XX
PN WO9845476-A1.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-GB00869.
XX
PR 08-APR-1997; 97GB-0007141.
XX
PA (FOOD-) FOOD RES INST.
XX
PI Schweizer M;
XX
DR WPI; 1999-024011/02.
XX
PT Assay for testing the carcinogenic properties of a test substance -
PT by introduction of a reporter gene expression vector containing a
PT repetitive DNA sequence that is unstable in cancer cells
XX
PS Disclosure; Page 17; 103pp; English.
XX
CC The present sequence represents an oligonucleotide used in the
CC construction of assay plasmids, which are used in the course of the
CC invention. The specification describes an assay for testing the
CC carcinogenic properties of a test substance. The assay comprises
CC introducing into cells a reporter gene expression vector comprising a
CC repetitive DNA sequence which exhibits instability in cancer cells,
CC whereby instability of the repetitive DNA sequence affects expression of
CC the reporter gene, exposing the resulting cells to the test substance
CC and determining whether the test substance is carcinogenic or
CC anti-carcinogenic by comparing the frequency of reporter gene expression
CC in the resulting cells with the frequency of reporter gene expression in
CC cells which have not been exposed to the test substance. The assay can
CC be used to identify human dietary components that protect against DNA
CC instability, and therefore some types of cancer, and can be used to
CC contribute to the scientific basis for a healthy diet.
XX
SQ Sequence 35 BP; 22 A; 5 C; 6 G; 2 T; 0 other;

```
  Query Match             0.6%;  Score 21.4;  DB 20;  Length 35;
  Best Local Similarity   80.6%;  Pred. No. 4e+04;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2561 cccagctttcttcttctttttttttttctgaa 2591
          ||  ||||| || || ||||||||||| |||
Db     33 CCGGGCTTTTTTTTTTTTTTTTTTTTCCGAA 3
```

Search completed: September 18, 2002, 01:22:27
Job time: 8329 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 22:25:53 ; Search time 77.81 Seconds
(without alignments)
11721.337 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacaggccgtggttagg.....aaactttaatgagttattta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22.6	0.6	45	3	US-08-718-904-50	Sequence 50, Appl
	2	22.6	0.6	45	5	PCT-US95-10973A-43	Sequence 43, Appl
	3	22.2	0.6	40	4	US-09-306-290-21	Sequence 21, Appl
	4	21.6	0.6	40	4	US-09-306-290-20	Sequence 20, Appl
c	5	21	0.6	43	2	US-08-686-599A-14	Sequence 14, Appl
	6	20.8	0.6	32	1	US-08-522-623-14	Sequence 14, Appl
	7	20.8	0.6	32	5	PCT-US93-03256-14	Sequence 14, Appl
c	8	20.6	0.6	45	4	US-09-389-341-65	Sequence 65, Appl
	9	20.4	0.5	50	2	US-08-316-439A-35	Sequence 35, Appl
c	10	20.2	0.5	34	6	5200340-28	Patent No. 5200340
c	11	20.2	0.5	40	1	US-08-208-486-57	Sequence 57, Appl
	12	20.2	0.5	46	1	US-08-284-784-17	Sequence 17, Appl
	13	20.2	0.5	46	2	US-08-854-811-17	Sequence 17, Appl
c	14	20.2	0.5	50	1	US-08-171-389-456	Sequence 456, App
	15	20.2	0.5	50	1	US-08-171-389-576	Sequence 576, App
	16	20.2	0.5	50	1	US-08-171-389-577	Sequence 577, App
c	17	20.2	0.5	50	1	US-08-420-443-1	Sequence 1, Appli
c	18	20.2	0.5	50	1	US-08-123-936-456	Sequence 456, App
	19	20.2	0.5	50	1	US-08-123-936-576	Sequence 576, App
	20	20.2	0.5	50	1	US-08-123-936-577	Sequence 577, App
c	21	20.2	0.5	50	2	US-08-475-228A-456	Sequence 456, App
	22	20.2	0.5	50	2	US-08-475-228A-576	Sequence 576, App
	23	20.2	0.5	50	2	US-08-475-228A-577	Sequence 577, App
c	24	20.2	0.5	50	3	US-08-482-080A-456	Sequence 456, App
	25	20.2	0.5	50	3	US-08-482-080A-576	Sequence 576, App
	26	20.2	0.5	50	3	US-08-482-080A-577	Sequence 577, App
c	27	20.2	0.5	50	5	PCT-US93-12388-456	Sequence 456, App
	28	20.2	0.5	50	5	PCT-US93-12388-576	Sequence 576, App
	29	20.2	0.5	50	5	PCT-US93-12388-577	Sequence 577, App
	30	20	0.5	30	1	US-08-318-193-64	Sequence 64, Appl
c	31	20	0.5	40	3	US-08-961-083-245	Sequence 245, App
	32	20	0.5	40	4	US-09-306-290-22	Sequence 22, Appl
	33	20	0.5	48	1	US-08-741-881-21	Sequence 21, Appl
	34	20	0.5	48	1	US-08-739-158-21	Sequence 21, Appl
	35	20	0.5	48	2	US-08-739-167-21	Sequence 21, Appl
	36	20	0.5	48	3	US-08-404-796-21	Sequence 21, Appl
	37	20	0.5	48	3	US-08-931-869-21	Sequence 21, Appl
	38	20	0.5	48	4	US-09-350-399-21	Sequence 21, Appl
	39	20	0.5	50	1	US-08-233-609-5	Sequence 5, Appli
	40	20	0.5	50	1	US-08-444-083-5	Sequence 5, Appli
	41	20	0.5	50	1	US-08-286-304-5	Sequence 5, Appli
	42	20	0.5	50	1	US-08-442-745-5	Sequence 5, Appli
	43	20	0.5	50	1	US-08-443-129-5	Sequence 5, Appli
	44	20	0.5	50	1	US-08-443-952-5	Sequence 5, Appli
	45	20	0.5	50	1	US-08-443-130-5	Sequence 5, Appli

ALIGNMENTS

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RESULT   1
US-08-718-904-50
; Sequence 50, Application US/08718904
; Patent No. 6037329
;  GENERAL INFORMATION:
;    APPLICANT:  Baird, J. Andrew
;    APPLICANT:  Chandler, Lois Ann
;    APPLICANT:  Sosnowski, Barbara A.
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
;    NUMBER OF SEQUENCES:  128
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/718,904
;      FILING DATE:  24-SEP-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6037329tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  760100.415C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..45
;      NAME/KEY:  (Ser4Gly)2
US-08-718-904-50


  Query Match              0.6%;  Score 22.6;  DB 3;  Length 45;
  Best Local Similarity   75.7%;  Pred. No. 1.7e+03;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;
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Qy    401 atggcgtcggcctcctccgggccgtcgtcttcggtcg 437
          ||||| ||| | || || ||  ||||||| |||| ||
Db      3 ATGGCCTCGTCGTCGTCGGGCTCGTCGTCGTCGGGCG 39


RESULT   2
PCT-US95-10973A-43
; Sequence 43, Application PC/TUS9510973A
;  GENERAL INFORMATION:
;    APPLICANT:  Prizm Pharmaceuticals, Inc.
;    TITLE OF INVENTION:  CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/10973A
;      FILING DATE:  29-AUG-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nottenburg, Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  760100.413PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..45
;      NAME/KEY:  (Ser4Gly)2
PCT-US95-10973A-43

  Query Match             0.6%;  Score 22.6;  DB 5;  Length 45;
  Best Local Similarity   75.7%;  Pred. No. 1.7e+03;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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          ||||| ||| | || || ||  ||||||| |||| ||
Db      3 ATGGCCTCGTCGTCGTCGGGCTCGTCGTCGTCGGGCG 39


RESULT   3
US-09-306-290-21
; Sequence 21, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
;  APPLICANT: Rovera, Giovanni
;  APPLICANT: Mukhopadhyay, Sunil
;  TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
;  TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
;  FILE REFERENCE: 09924-10
;  CURRENT APPLICATION NUMBER: US/09/306,290
;  CURRENT FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer p41
;   OTHER INFORMATION: FH92
US-09-306-290-21


  Query Match             0.6%;  Score 22.2;  DB 4;  Length 40;
  Best Local Similarity   77.1%;  Pred. No. 2.1e+03;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2568 ttcttcttcttttttttttctgaaaaaaggaaaaa 2602
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Db      1 ttttttttttttttttttttttgaaaagctggaaaa 35


RESULT   4
US-09-306-290-20
; Sequence 20, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
;  APPLICANT: Rovera, Giovanni
;  APPLICANT: Mukhopadhyay, Sunil
;  TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
;  TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
;  FILE REFERENCE: 09924-10
;  CURRENT APPLICATION NUMBER: US/09/306,290
;  CURRENT FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer p41
;   OTHER INFORMATION: FH46
US-09-306-290-20


  Query Match             0.6%;  Score 21.6;  DB 4;  Length 40;
  Best Local Similarity   75.0%;  Pred. No. 3.1e+03;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttcttttttttttctgaaaaaaggaaaaa 2602
           ||| || || |||||||||| | || |  || |||
Db      1 ttttttttttttttttttttcgggaacatagagaaa 36


RESULT   5
US-08-686-599A-14/c
; Sequence 14, Application US/08686599A
; Patent No. 5891439
;  GENERAL INFORMATION:
;    APPLICANT:  Olsson, Thomas
;    APPLICANT:  Vaidya, Tushar
;    APPLICANT:  Bakhiet, Abdel-Moiz
;    APPLICANT:  Kristensson, Krister
;    APPLICANT:  Donelson, John E.
;    TITLE OF INVENTION:  LYMPHOCYTE STIMULATING FACTOR
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS, LLP
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314-3187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/686,599A
;       FILING DATE:  26-JUL-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Duffett, Benton S.
;       REGISTRATION NUMBER:  22,030
;       REFERENCE/DOCKET NUMBER:  003300-383
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  43 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  TLTF
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..42
US-08-686-599A-14

  Query Match             0.6%;  Score 21;  DB 2;  Length 43;
  Best Local Similarity   73.0%;  Pred. No. 5e+03;
  Matches   27;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttcttttttttttctgaaaaaaggaaaaag 2603
          ||| || || |||||||||  |||||  |  | ||||
Db     42 TTTTTTTTTTTTTTTTTTTAGTGAAATGACAATAAAG 6


RESULT   6
US-08-522-623-14
; Sequence 14, Application US/08522623
; Patent No. 5585242
;  GENERAL INFORMATION:
;    APPLICANT:  Khalil, Omar S.
;    APPLICANT:  Bouma, Stanley R.
;    APPLICANT:  Pabich, Edward K.
;    TITLE OF INVENTION:  METHOD AND DEVICE FOR DETECTION OF
;    TITLE OF INVENTION:  NUCLEIC ACID OR ANALYTE USING TOTAL INTERNAL REFLECTION
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/522,623
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,839
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/863,553
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brainard, Thomas D.
;      REGISTRATION NUMBER:  32,459
;      REFERENCE/DOCKET NUMBER:  5158.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 937-4884
;      TELEFAX:  (708) 937-9556
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  32
US-08-522-623-14


  Query Match             0.6%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   78.1%;  Pred. No. 4.7e+03;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2555 ccacctcccagctttcttcttcttttttttttt 2586
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Db      1 CCGCCTGTCCGCTTTTTTTTTTTTTTTTTTT 32


RESULT   7
PCT-US93-03256-14
; Sequence 14, Application PC/TUS9303256
;  GENERAL INFORMATION:
;    APPLICANT:  Abbott Laboratories
;    TITLE OF INVENTION:  METHOD AND DEVICE FOR DETECTION OF
;    TITLE OF INVENTION:  NUCLEIC ACID OR ANALYTE USING TOTAL INTERNAL REFLECTION
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn and WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/03256
;      FILING DATE:  19930506
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/863,553
;      FILING DATE:  06 APRIL 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brainard, Thomas D.
;      REGISTRATION NUMBER:  32,459
;      REFERENCE/DOCKET NUMBER:  5158.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 937-4884
;      TELEFAX:  (708) 937-2623
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  32
PCT-US93-03256-14


  Query Match             0.6%;  Score 20.8;  DB 5;  Length 32;
  Best Local Similarity   78.1%;  Pred. No. 4.7e+03;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;
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Qy   2555 ccacctcccagctttcttcttctttttttttt 2586
          || |||  | ||||| || || ||||||||||
Db      1 CCGCCTGTCCGCTTTTTTTTTTTTTTTTTTT 32


RESULT   8
US-09-389-341-65/c
; Sequence 65, Application US/09389341
; Patent No. 6200803
; GENERAL INFORMATION:
;  APPLICANT: Roberts, Christopher J.
;  TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
;  TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATIVE
;  TITLE OF INVENTION: DRUGS
;  FILE REFERENCE: 9301-057
;  CURRENT APPLICATION NUMBER: US/09/389,341
;  CURRENT FILING DATE: 1999-09-02
;  EARLIER APPLICATION NUMBER: 09/315,794
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-389-341-65


  Query Match             0.6%;  Score 20.6;  DB 4;  Length 45;
  Best Local Similarity   67.4%;  Pred. No. 6.8e+03;
  Matches   29;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   3015 catcttttccaacagtgttctcctgtttgtggagctaaggtaa 3057
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Db     45 CATTTTTTCTGCCAGTGTTCTCCTGCGCTTTTGGATATGATAA 3


RESULT   9
US-08-316-439A-35
; Sequence 35, Application US/08316439A
; Patent No. 5840520
;  GENERAL INFORMATION:
;    APPLICANT:  CLARKE, DAVID KIRKWOOD
;    APPLICANT:  PALESE, PETER M
;    TITLE OF INVENTION:  RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
;    TITLE OF INVENTION:  SYSTEMS
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOLEY GODWARD CASTRO HUDDLESON & TATUM
;      STREET:  FIVE PALO ALTO SQUARE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/316,439A
;      FILING DATE:  September 30, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/190,678
;      FILING DATE:  February 1, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/925,061
;      FILING DATE:  August 4, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/527,237
;      FILING DATE:  May 22, 1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/440,053
;      FILING DATE:  No. 5840520ember 21, 1989
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/399,728
;      FILING DATE:  August 28, 1989
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CSERR, LUANN
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  AVIR-010/00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 843-5165
;      TELEFAX:  (415) 857-0663
;      TELEX:  380816 COOLEY PA
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  SYNTHETIC DNA
US-08-316-439A-35


  Query Match             0.5%;  Score 20.4;  DB 2;  Length 50;
  Best Local Similarity   65.2%;  Pred. No. 8.4e+03;
  Matches   30;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   3642 tgttcagaaatggcaaatacaatataaaagtgatatatggttttaa 3687
          | ||||   || |  | || ||  ||||| | |||||   ||||||
Db      2 TATTCAATTATAGTTATTAAAAATTAAAAATCATATAATTTTTTAA 47


RESULT  10
5200340-28/c
;Patent No. 5200340
;    APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
;    TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
;ACTIVATORS
;    NUMBER OF SEQUENCES: 34
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/53,412
;      FILING DATE: 22-MAY-1987
;SEQ ID NO:28:
;      LENGTH: 34
5200340-28


  Query Match             0.5%;  Score 20.2;  DB 6;  Length 34;
  Best Local Similarity   75.8%;  Pred. No. 7.4e+03;
  Matches   25;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    333 cgattccgagaagaggaagaaccggattgaaag 365
          ||| ||||| |||| |||||| ||   ||| ||
Db     33 CGACTCCGACAAGAAGAAGAAGCGACATGACAG 1


RESULT  11
US-08-208-486-57/c
; Sequence 57, Application US/08208486
; Patent No. 5389531
;  GENERAL INFORMATION:
;    APPLICANT:  Ito, Junetsu
;    APPLICANT:  Yoo, Seung-Ku
;    TITLE OF INVENTION:  METHODS TO REPLICATE DNA in vitro USING
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;    TITLE OF INVENTION:  PRD1-CATALYZED DNA REPLICATION SYSTEMS
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cahill, Sutton & Thomas
;      STREET:  155 Park One, 2141 E. Highland Ave.
;      CITY:  Phoenix
;      STATE:  Arizona
;      COUNTRY:  U.S.A.
;      ZIP:  85016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 1.2 Mb
;      COMPUTER:  Packard Bell (IBM PC/AT compatible)
;      OPERATING SYSTEM:  MS-Dos, Version 5.0
;      SOFTWARE:  WordPerfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,486
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/869,916
;      FILING DATE:  April 14, 1992
;      APPLICATION NUMBER:  Japan 240525/91
;      FILING DATE:  August 26, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janelle Faunce Raupp
;      REGISTRATION NUMBER:  30,485
;      REFERENCE/DOCKET NUMBER:  #3954-A-7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (602) 956-7000
;      TELEFAX:  (602) 495-9475
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
US-08-208-486-57


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; Sequence 17, Application US/08284784
; Patent No. 5629172
;  GENERAL INFORMATION:
;    APPLICANT:  MASCARENHAS, DESMOND
;    APPLICANT:  ZHANG, YANG
;    APPLICANT:  OLSON, PAMELA S.
;    APPLICANT:  OLSEN, DAVID R.
;    APPLICANT:  CARRILLO, PEDRO A.
;    TITLE OF INVENTION:  EXPRESSION OF FUSION POLYPEPTIDES
;    TITLE OF INVENTION:  TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,784
;      FILING DATE:  02-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  22095-20275.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-284-784-17


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RESULT  13
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; Sequence 17, Application US/08854811
; Patent No. 5914254
;  GENERAL INFORMATION:
;    APPLICANT:  Mascarenhas, Desmond
;    APPLICANT:  Zhang, Yang
;    APPLICANT:  Olson, Pamela S.
;    APPLICANT:  Olsen, David R.
;    APPLICANT:  Cohen, Pedro A.
;    TITLE OF INVENTION:  EXPRESSION OF FUSION POLYPEPTIDES
;    TITLE OF INVENTION:  TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
;    TITLE OF INVENTION:  SEQUENCES
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/854,811
;      FILING DATE:  12-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284,784
;      FILING DATE:  02-AUG-1994
;      APPLICATION NUMBER:  08/100,744
;      FILING DATE:  02-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Buffinger, Nicholas S
;      REGISTRATION NUMBER:  39,124
;      REFERENCE/DOCKET NUMBER:  22095-20275.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
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;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-854-811-17


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; Sequence 456, Application US/08171389
; Patent No. 5578444
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/171,389
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175/G19P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  456:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human beta-LH gene
US-08-171-389-456


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  Matches   31;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

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RESULT  15
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; Sequence 576, Application US/08171389
; Patent No. 5578444
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175/G19P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  576:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
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US-08-171-389-576


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  Matches   25;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

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GenCore version 4.5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5		23.8	0.6	50	29	US-09-755-374A-17699	Sequence 17699, A
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23		22.6	0.6	45	6	US-08-213-447A-43	Sequence 43, Appl
24		22.6	0.6	45	6	US-08-297-961A-43	Sequence 43, Appl
25		22.6	0.6	45	7	US-08-305-771A-43	Sequence 43, Appl
26		22.6	0.6	45	10	US-08-672-353-40	Sequence 40, Appl
27		22.6	0.6	45	12	US-08-805-382-29	Sequence 29, Appl
28		22.6	0.6	45	12	US-08-805-383-29	Sequence 29, Appl
29		22.6	0.6	45	18	US-09-449-249-50	Sequence 50, Appl
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31		22.6	0.6	45	33	US-09-861-257-29	Sequence 29, Appl

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c	40	22.2	0.6	48	22	US-09-572-021-4910	Sequence 4910, Ap
c	41	22.2	0.6	48	37	US-10-017-974-35315	Sequence 35315, A
	42	22.2	0.6	50	7	US-08-326-514-10	Sequence 10, Appl
c	43	22.2	0.6	50	11	US-08-798-074-3200	Sequence 3200, Ap
c	44	22.2	0.6	50	11	US-08-798-074B-3200	Sequence 3200, Ap
	45	22.2	0.6	50	29	US-09-755-374A-2636	Sequence 2636, Ap

ALIGNMENTS

```
RESULT   1
US-10-003-354-6
; Sequence 6, Application US/10003354
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0348
;  CURRENT APPLICATION NUMBER: US/10/003,354
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 6
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Probe
US-10-003-354-6


  Query Match             0.7%;  Score 26;  DB 37;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     301 cgcgggttctgtaaagagacgttggg 326
           ||||||||||||||||||||||||||
Db       1 cgcgggttctgtaaagagacgttggg 26


RESULT   2
US-09-755-374A-25691
; Sequence 25691, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 25691
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (25692 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg44004721
US-09-755-374A-25691


  Query Match             0.7%;  Score 25;  DB 29;  Length 50;
  Best Local Similarity   69.4%;  Pred. No. 1.4e+05;
  Matches   34;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    3479 ttttttttttcataatttactatttatgatgtatttaagtgttttattaa 3527
           |||||||||  |  |||  | ||||  || | || ||  | ||||||||
Db       1 ttttttttttttttttttttttttttagcatttttttaaatggctttattaa 49


RESULT   3
US-09-342-217-4074
; Sequence 4074, Application US/09342217
;  GENERAL INFORMATION:
;    APPLICANT:  Craig A. Rosen, et. al.
;    TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products - PO40
;    NUMBER OF SEQUENCES:  5660
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/342,217
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PO40
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  4074:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs.
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-342-217-4074


  Query Match             0.7%;  Score 24.4;  DB 17;  Length 50;
  Best Local Similarity   73.7%;  Pred. No. 2e+05;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2562 ccagctttcttcttctttttttttttctgaaaaaaggaa 2599
           | || ||| || || ||||||||||   ||||||  ||
Db      13 CGAGTTTTTTTTTTTTTTTTTTTTNANAAAAAANNAA 50


RESULT   4
US-09-342-217A-4074
; Sequence 4074, Application US/09342217A
; GENERAL INFORMATION:
;  APPLICANT:  Rosen, Craig, et al.
;  TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products 40
;  FILE REFERENCE:  PO-40
;  CURRENT APPLICATION NUMBER: US/09/342,217A
;  CURRENT FILING DATE:  1999-06-29
```

```
;  PRIOR APPLICATION NUMBER:  60/091,170
;  PRIOR FILING DATE:  1998-06-30
;  NUMBER OF SEQ ID NOS:  5662
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4074
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (38)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (40)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (47)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (48)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-342-217A-4074


 Query Match             0.7%;  Score 24.4;  DB 17;  Length 50;
 Best Local Similarity   73.7%;  Pred. No. 2e+05;
 Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2562 ccagctttcttcttctttttttttttctgaaaaaaggaa 2599
          | || ||| || || ||||||||||   ||||||  ||
Db     13 cgagtttttttttttttttttttttnanaaaaaannaa 50


RESULT   5
US-09-755-374A-17699
; Sequence 17699, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 17699
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (17700 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(26)
;   OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg43932310
US-09-755-374A-17699


  Query Match             0.6%;  Score 23.8;  DB 29;  Length 50;
  Best Local Similarity   72.1%;  Pred. No. 2.8e+05;
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   3470 ttcttgctatttttttttcataatttactatttatgatgtatt 3512
          || ||  | ||||||||| |  | ||| ||||||  || ||||
Db      7 ttttttttttttttttttagcacttagtatttagcatttatt 49


RESULT   6
US-09-396-196F-83096
; Sequence 83096, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83096
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196F-83096


  Query Match             0.6%;  Score 23.4;  DB 17;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.5e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2110 agcccttgccccagcaatgctgaat 2134
          |||||||||||||| ||||||||||
Db      1 agcccttgccccaggaatgctgaat 25


RESULT   7
US-08-401-791A-15261
; Sequence 15261, Application US/08401791A
;  GENERAL INFORMATION:
;    APPLICANT:  Haseltine, William
;    APPLICANT:  Rosen, Craig
;    APPLICANT:  Ruben, Steve
;    APPLICANT:  Dillon, Patrick
;    APPLICANT:  Li, Haodong
;    APPLICANT:  Earle-Hughes, Julie
;    TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products
;    NUMBER OF SEQUENCES:  17621
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 5.0
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,791A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  325800-307
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 994-1700
;      TELEFAX:  (201) 994-1744
;  INFORMATION FOR SEQ ID NO:  15261:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-401-791A-15261


  Query Match             0.6%;  Score 23.4;  DB 8;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+05;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttctttttttttttctgaaaaaaggaaaaa 2602
          ||| || || |||||||||| | ||||||  |  ||
Db     15 TTTTTTTTTTTTTTTTTTTTTNAAAAAAAAANNAA 50


RESULT   8
US-08-401-791B-15261
; Sequence 15261, Application US/08401791B
;  GENERAL INFORMATION:
;    APPLICANT:  Haseltine, William A.
;    APPLICANT:  Rosen, Craig A.
;    APPLICANT:  Ruben, Steven M.
;    APPLICANT:  Dillon, Patrick J.
;    APPLICANT:  Li, Haodong
;    APPLICANT:  Earle-Hughes, Julie
;    TITLE OF INVENTION:  Human Genes, Sequences and Expression Products - 18
;    NUMBER OF SEQUENCES:  17623
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,791B
;      FILING DATE:  March 10, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele M. Wales
;      REGISTRATION NUMBER:  P-43,975
;      REFERENCE/DOCKET NUMBER:  PO-18
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8439
;  INFORMATION FOR SEQ ID NO:  15261:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-401-791B-15261


  Query Match             0.6%;  Score 23.4;  DB 8;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+05;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2567 tttcttcttctttttttttttctgaaaaaaggaaaaa 2602
          ||| || || |||||||||| | ||||||  |  ||
Db     15 TTTTTTTTTTTTTTTTTTTTTNAAAAAAAAANNAA 50


RESULT   9
US-09-755-374A-2381
; Sequence 2381, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and M
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 2381
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (2382 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(26)
;   OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg43928213
US-09-755-374A-2381


  Query Match             0.6%;  Score 23.4;  DB 29;  Length 50;
  Best Local Similarity   67.3%;  Pred. No. 3.6e+05;
  Matches   33;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   2565 gctttcttcttcttttttttttctgaaaaaaggaaaaagcacacagcac 2613
          | || ||| || |||||||||| |  |||| | | |||  |   | |||
Db      1 gtttccttttttttttttttttttgaaaatgtacaaaatatctatcac 49


RESULT  10
US-09-755-374A-25692
; Sequence 25692, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and M
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 25692
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(0)
;   OTHER INFORMATION: 2 of 2 allelic variants (25691 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg44004721
US-09-755-374A-25692


  Query Match             0.6%;  Score 23.4;  DB 29;  Length 50;
  Best Local Similarity   67.3%;  Pred. No. 3.6e+05;
  Matches   33;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   3479 ttttttttcataatttactatttatgatgtatttaagtgttttattaa 3527
          |||||||||  |  |||  | |||   || | || ||  | ||||||||
Db      1 ttttttttttttttttttttttttgcatttttaaatggctttattaa 49
```

```
RESULT  11
PCT-US01-47856-5024/c
; Sequence 5024, Application PC/TUS0147856
; GENERAL INFORMATION:
;  APPLICANT: BIOCARDIA, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Quertermous, Thomas
;  APPLICANT:  Johnson, Frances
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Matcuk, George
;  APPLICANT:  Prentice, James
;  APPLICANT:  Phillips, Julie
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Altman, Peter
;  TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
;  FILE REFERENCE: 506612000140
;  CURRENT APPLICATION NUMBER: PCT/US01/47856
;  CURRENT FILING DATE:  2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/241,994
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 8832
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5024
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US01-47856-5024


  Query Match             0.6%;  Score 23.2;  DB 1;  Length 50;
  Best Local Similarity   70.5%;  Pred. No. 4e+05;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1214 gacttcttacaagacatccctgatggtctttttttggatgctga 1257
          || | | || |||| ||| |  | ||| ||| ||||| ||| ||
Db     44 GAATGCCTATAAGAAATCTCAAAAGGTATTTGTTTGGGTGCAGA 1


RESULT  12
US-09-755-374A-6837/c
; Sequence 6837, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 6837
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (6838 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(26)
;   OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg44911096
US-09-755-374A-6837


  Query Match             0.6%;  Score 23.2;  DB 29;  Length 50;
  Best Local Similarity   77.8%;  Pred. No. 4e+05;
  Matches   28;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2555 ccacctcccagctttcttcttcttttttttttctga 2590
           |||   ||||| ||| | ||| ||||||||||| |
Db     44 CCAAACCCCAGATTTGTACTTTTTTTTTTTTCTAA 9


RESULT  13
US-09-755-374A-13433
; Sequence 13433, Application US/09755374A
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and M
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/09/755,374A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 13433
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (13434 is other entry)
;   NAME/KEY: misc_feature
;   LOCATION: (25)...(26)
;   OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg44002450
US-09-755-374A-13433


  Query Match             0.6%;  Score 23.2;  DB 29;  Length 50;
  Best Local Similarity   77.8%;  Pred. No. 4e+05;
  Matches   28;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2563 cagctttcttcttcttttttttttctgaaaaaagga 2598
           ||||||| || || |||||||||    ||||||| |
Db     15 cagctttttttttttttttttttaaataaaaaagca 50


RESULT  14
US-08-346-731-6670
; Sequence 6670, Application US/08346731
;  GENERAL INFORMATION:
;    APPLICANT:  Craig A. Rosen, et. al.
;    TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products - PO16
;    NUMBER OF SEQUENCES:  12477
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,731
;      FILING DATE:
;      CLASSIFICATION:  435
```

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PO16
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  6670:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-346-731-6670


  Query Match             0.6%;  Score 23;  DB 7;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   2556 cacctcccagctttcttcttctttttttttttctgaaaaaaggaaaaag 2603
          ||   |||   ||| || || |||||||||| |   ||||  |||| |
Db      3 CANAGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAAAAGG 50


RESULT  15
US-08-420-856-6670
; Sequence 6670, Application US/08420856
;  GENERAL INFORMATION:
;    APPLICANT:  Rosen, Craig A.
;    APPLICANT:  Ruben, Steve M.
;    APPLICANT:  Dillon, Patrick J.
;    APPLICANT:  Li, Haodong
;    APPLICANT:  Haseltine, William A.
;    TITLE OF INVENTION:  Human Genes, Sequences, and Expression Products - 16
;    NUMBER OF SEQUENCES:  12477
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 5.0
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/420,856
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  325800-259
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 994-1700
;      TELEFAX:  (201) 994-1744
;  INFORMATION FOR SEQ ID NO:  6670:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-420-856-6670


  Query Match             0.6%;  Score 23;  DB 8;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   2556 cacctcccagctttcttcttctttttttttctgaaaaaaggaaaaag 2603
          ||   |||   ||| || || |||||||||| |   ||||  |||| |
Db      3 CANAGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAAAAGG 50


Search completed:  September 18, 2002, 02:37:20
Job time:  9827 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 23:59:13 ; Search time 655.22 Seconds
(without alignments)
18027.320 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacaggccgtggttagg.....aaactttaatgagttattta 3713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2122332 seqs, 1590608744 residues

Total number of hits satisfying chosen parameters: 1036418

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		23.4	0.6	25	5	US-09-396-196G-83096	Sequence 83096, A
2	c	23.2	0.6	50	6	US-10-131-831-5024	Sequence 5024, Ap
3		22.6	0.6	45	6	US-10-189-360-50	Sequence 50, Appl
4		22.4	0.6	25	5	US-09-396-196G-83095	Sequence 83095, A
5	c	22	0.6	50	6	US-10-131-831-7656	Sequence 7656, Ap
6		21.8	0.6	25	5	US-09-396-196G-83082	Sequence 83082, A
7		21.8	0.6	25	5	US-09-396-196G-83089	Sequence 83089, A
8	c	21.6	0.6	50	6	US-10-131-831-4391	Sequence 4391, Ap
9	c	21.4	0.6	43	7	US-10-027-632-177610	Sequence 177610,
10	c	21.4	0.6	43	7	US-10-027-632-177620	Sequence 177620,
11		21.4	0.6	50	6	US-10-131-831-4588	Sequence 4588, Ap
12		21.2	0.6	46	7	US-10-055-728-32	Sequence 32, Appl
13	c	21	0.6	43	7	US-10-027-632-177600	Sequence 177600,
14		21	0.6	47	7	US-10-170-097-805	Sequence 805, App
15	c	21	0.6	48	7	US-10-156-306-7691	Sequence 7691, Ap
16		21	0.6	50	6	US-10-131-831-2704	Sequence 2704, Ap
17	c	21	0.6	50	6	US-10-131-831-3010	Sequence 3010, Ap
18	c	21	0.6	50	6	US-10-131-831-3861	Sequence 3861, Ap
19	c	20.6	0.6	40	5	US-09-914-101-10	Sequence 10, Appl
20	c	20.6	0.6	50	5	US-09-718-321A-50	Sequence 50, Appl
21	c	20.4	0.5	44	7	US-10-027-632-75768	Sequence 75768, A
22		20.4	0.5	46	7	US-10-170-097-1292	Sequence 1292, Ap
23	c	20.4	0.5	48	5	US-09-745-237A-4329	Sequence 4329, Ap
24		20.4	0.5	50	5	US-09-923-070A-6	Sequence 6, Appli
25		20.4	0.5	50	5	US-09-724-379A-6	Sequence 6, Appli
26	c	20.4	0.5	50	6	US-10-131-831-391	Sequence 391, App
27		20.2	0.5	25	5	US-09-396-196G-83088	Sequence 83088, A
28		20.2	0.5	25	5	US-09-396-196G-83097	Sequence 83097, A
29	c	20.2	0.5	25	5	US-09-396-196G-92147	Sequence 92147, A
30	c	20.2	0.5	36	4	US-08-705-477E-68	Sequence 68, Appl
31	c	20.2	0.5	47	5	US-09-702-498A-23	Sequence 23, Appl
32		20.2	0.5	47	5	US-09-702-498A-24	Sequence 24, Appl
33		20.2	0.5	47	7	US-10-170-097-1167	Sequence 1167, Ap
34	c	20.2	0.5	48	5	US-09-730-289B-1167	Sequence 1167, Ap
35	c	20.2	0.5	48	7	US-10-156-306-7172	Sequence 7172, Ap
36	c	20.2	0.5	50	5	US-09-886-492-3196	Sequence 3196, Ap
37		20.2	0.5	50	6	US-10-131-831-3607	Sequence 3607, Ap
38	c	20.2	0.5	50	6	US-10-131-831-4502	Sequence 4502, Ap
39		20.2	0.5	50	7	US-10-097-105-1012	Sequence 1012, Ap
40	c	20	0.5	40	4	US-08-961-083-245	Sequence 245, App
41		20	0.5	47	7	US-10-170-097-804	Sequence 804, App
42	c	20	0.5	48	5	US-09-730-289B-1326	Sequence 1326, Ap
43		20	0.5	48	5	US-09-503-138B-21	Sequence 21, Appl
44		20	0.5	48	7	US-10-150-407-21	Sequence 21, Appl
45	c	20	0.5	48	7	US-10-156-306-7182	Sequence 7182, Ap

ALIGNMENTS

RESULT 1
US-09-396-196G-83096
; Sequence 83096, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83096

Query Match 0.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 5e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2110 agcccttgccccagcaatgctgaat 2134
||||||||||||||| ||||||||||
Db 1 agcccttgccccaggaatgctgaat 25

RESULT 2
US-10-131-831-5024/c
; Sequence 5024, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764

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;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9190
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5024
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-831-5024


  Query Match             0.6%;  Score 23.2;  DB 6;  Length 50;
  Best Local Similarity   70.5%;  Pred. No. 7.4e+04;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1214 gacttcttacaagacatccctgatggtctttttttggatgctga 1257
          || | | || |||| ||| |  | ||| ||| ||||| ||| ||
Db     44 GAATGCCTATAAGAAATCTCAAAAGGTATTTGTTTGGGTGCAGA 1


RESULT   3
US-10-189-360-50
; Sequence 50, Application US/10189360
;   GENERAL INFORMATION:
;        APPLICANT: Baird, J. Andrew
;                   Chandler, Lois Ann
;                   Sosnowski, Barbara A.
;        TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
;                            FOR THERAPE
;        NUMBER OF SEQUENCES: 128
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/189,360
;             FILING DATE: 02-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/718,904
;             FILING DATE: 24-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Nottenburg Ph.D., Carol
;             REGISTRATION NUMBER: 39,317
;             REFERENCE/DOCKET NUMBER: 760100.415C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;    INFORMATION FOR SEQ ID NO: 50:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 45 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  (Ser4Gly)2
;             LOCATION:  3..45
;        SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-189-360-50


  Query Match             0.6%;  Score 22.6;  DB 6;  Length 45;
  Best Local Similarity   75.7%;  Pred. No. 1e+05;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    401 atggcgtcggcctcctccgggccgtcgtcttcggtcg 437
          ||||| ||| | || || ||  ||||||| |||| ||
Db      3 ATGGCCTCGTCGTCGTCGGGCTCGTCGTCGTCGGGCG 39


RESULT   4
US-09-396-196G-83095
; Sequence 83095, Application US/09396196G
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83095
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-83095


  Query Match             0.6%;  Score 22.4;  DB 5;  Length 25;
  Best Local Similarity   95.8%;  Pred. No. 8.9e+04;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2057 agcctcagaagacctggaacaaga 2080
          |||||||||||||||| |||||||
Db      2 agcctcagaagacctgaaacaaga 25


RESULT   5
US-10-131-831-7656/c
; Sequence 7656, Application US/10131831
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;  TITLE OF INVENTION:  TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000121
;  CURRENT APPLICATION NUMBER: US/10/131,831
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9190
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7656
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-831-7656


  Query Match             0.6%;  Score 22;  DB 6;  Length 50;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+05;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   1638 gagacactgtctcagtgcatcgcccaggct 1667
          ||||||  |||||| || || |||||||||
Db     48 GAGACAGGGTCTCACTGTATTGCCCAGGCT 19


RESULT   6
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US-09-396-196G-83082
; Sequence 83082, Application US/09396196G
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83082
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-83082


  Query Match             0.6%;  Score 21.8;  DB 5;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 1.3e+05;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   2002 tacaaccttggaaaagcttgaagtt 2026
           | ||||||||||||||||||| |||
Db      1 ttcaaccttggaaaagcttgatgtt 25


RESULT   7
US-09-396-196G-83089
; Sequence 83089, Application US/09396196G
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83089
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-83089


  Query Match             0.6%;  Score 21.8;  DB 5;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 1.3e+05;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   2432 actcttaatttcctcaggacagact 2456
           |||||| |||||||||||||| ||||
Db      1 actcttcatttcctcaggacggact 25


RESULT   8
US-10-131-831-4391/c
; Sequence 4391, Application US/10131831
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;  TITLE OF INVENTION:  TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000121
;  CURRENT APPLICATION NUMBER: US/10/131,831
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9190
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4391
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-831-4391


  Query Match             0.6%;  Score 21.6;  DB 6;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+05;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2607 acagcacacaatttcaagccattttcagatcagaac 2642
           |||    |||||||| |   |||||||||||||| ||
Db     50 ACATGGAACAATTTCCAAGAATTTTCAGATCAGGAC 15


RESULT   9
US-10-027-632-177610/c
; Sequence 177610, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177610
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-177610


  Query Match             0.6%;  Score 21.4;  DB 7;  Length 43;
  Best Local Similarity   71.8%;  Pred. No. 2e+05;
  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2939 ggttgtttttctaaatgtgaagacttaccaaatgaattt 2977
           | || || || | | |||||| | ||| ||  |||||||
Db     39 GCTTTTTGTTATGAGTGTGAACATTTATCACTTGAATTT 1


RESULT  10
US-10-027-632-177620/c
; Sequence 177620, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177620
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-177620


  Query Match             0.6%;  Score 21.4;  DB 7;  Length 43;
  Best Local Similarity   71.8%;  Pred. No. 2e+05;
  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2939 ggttgtttttctaaatgtgaagacttaccaaatgaattt 2977
           | || || || | | |||||| | ||| ||  |||||||
Db     39 GCTTTTTGTTATGAGTGTGAACATTTATCACTTGAATTT 1


RESULT  11
US-10-131-831-4588
; Sequence 4588, Application US/10131831
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;  TITLE OF INVENTION:  TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000121
;  CURRENT APPLICATION NUMBER: US/10/131,831
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9190
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4588
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-831-4588


  Query Match             0.6%;  Score 21.4;  DB 6;  Length 50;
  Best Local Similarity   80.6%;  Pred. No. 2.1e+05;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   3247 acaagagttgtggttttccatctgatccttc 3277
           |||  |||| ||||||||||||| |||  ||
Db     17 acataagttatggttttccatcttatctgtc 47


RESULT  12
US-10-055-728-32
; Sequence 32, Application US/10055728
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER:.60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligo (dT) primer with a 5' M13 tail
US-10-055-728-32


  Query Match             0.6%;  Score 21.2;  DB 7;  Length 46;
  Best Local Similarity   69.0%;  Pred. No. 2.3e+05;
  Matches   29;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   2547 gtgtttaaccacctcccagctttcttcttctttttttttttct 2588
           ||  | || |  |  |||| ||| || || ||||||||||| |
Db      4 gttgtaaaacgacggccagttttttttttttttttttttttt 45


RESULT  13
US-10-027-632-177600/c
; Sequence 177600, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177600
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-177600


  Query Match             0.6%;  Score 21;  DB 7;  Length 43;
  Best Local Similarity   69.2%;  Pred. No. 2.5e+05;
  Matches   27;  Conservative    1;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2939 ggttgtttttctaaatgtgaagacttaccaaatgaattt 2977
           | || || || | | |||||| : ||| ||  |||||||
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Db      39 GCTTTTTGTTATGAGTGTGAACRTTTATCACTTGAATTT 1


RESULT  14
US-10-170-097-805
; Sequence 805, Application US/10170097
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
;  TITLE OF INVENTION:  GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
;  FILE REFERENCE: GEN-T114XC2D1
;  CURRENT APPLICATION NUMBER: US/10/170,097
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: US 09/641,638
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: US 09/502,330
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: US 60/133,200
;  PRIOR FILING DATE: 1999-05-07
;  PRIOR APPLICATION NUMBER: US 09/275,267
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: US 60/119,917
;  PRIOR FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 1304
;  SOFTWARE: Patent.pm
; SEQ ID NO 805
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 12-740-118 : polymorphic base C or T
US-10-170-097-805


  Query Match             0.6%;  Score 21;  DB 7;  Length 47;
  Best Local Similarity   65.9%;  Pred. No. 2.6e+05;
  Matches   27;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    948 tccaacataaagaggcggaatttctgcagaagctgcttcca 988
          |||| || ||| ||: |||| | |   ||| || | |||| |
Db      4 tccaccaaaaaaagrgggaayctaaccaggaggtccttcaa 44


RESULT  15
US-10-156-306-7691/c
; Sequence 7691, Application US/10156306
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of IKK-Gamma and PKR
;  FILE REFERENCE: MBHB01-664-A (400/050)
;  CURRENT APPLICATION NUMBER: US/10/156,306
;  CURRENT FILING DATE:  2002-05-28
;  NUMBER OF SEQ ID NOS: 8013
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7691
;   LENGTH: 48
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-10-156-306-7691


  Query Match             0.6%;  Score 21;  DB 7;  Length 48;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+05;
  Matches   30;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    411 cctcctccgggccgtcgtcttcggtcggtttttcatcctttgatc 455
          ||| |||| || ||  ||| | |   ||  |||| |||| || ||
Db     46 CCTTCTCCCGGACGATGTCCTTGAAGGGAGTTTCCTCCTCTGCTC 2


Search completed: September 18, 2002, 02:48:37
Job time: 10164 sec
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